LISTING OF THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Previously Presented) A method for detecting a polymorphism related to a genetic disease in a patient sample nucleic acid, comprising the steps of:

providing the patient sample nucleic acid containing a first and a second loci having a first and second polymorphism, respectively, related to the genetic disease at a microarray site;

providing an unlabeled blocker that is complementary to the first locus containing the first polymorphism related to the genetic disease;

hybridizing the unlabeled blocker with the first locus such that the first polymorphism is blocked by the unlabeled blocker, wherein the second locus is unblocked;

providing a detectable discriminator that is capable of hybridizing with the second locus containing the second polymorphism related to the genetic disease;

hybridizing the detectable discriminator with the second locus containing the second polymorphism related to the genetic disease; and

detecting the second polymorphism related to the genetic disease by detecting the presence of the discriminator at the microarray site.

2-5. (Canceled)

6. (Previously Presented) The method of claim 1, wherein the microarray site comprises a site of an actively addressable electronic microarray.

7. (Previously Presented) The method of claim 6, wherein the addressable electronic microarray includes a permeation layer.

8. (Previously Presented) The method of claim 1, wherein the patient sample is amplified.

9. (Previously Presented) The method of claim 8, wherein the amplification includes polymerase chain reaction (PCR).

10. (Withdrawn-Previously Presented) The method of claim 8, wherein the amplification includes ligase chain reaction (LCR).

11. (Withdrawn- Previously Presented) The method of claim 8, wherein the amplification includes strand displacement amplification (SDA).

12. (Withdrawn- Previously Presented) The method of claim 8, wherein the amplification includes the transcription-based amplification system (TAS).

13. (Withdrawn- Previously Presented) The method of claim 8, wherein the amplification includes the self-sustained sequence replication system (3SR).

14. (Withdrawn- Previously Presented) The method of claim 8, wherein the amplification includes the Qβ replicase amplification system (Qβ).

15-17. (Canceled)

18. (Previously Presented) The method of claim 1, further includes the step of performing a screening step.

19. (Previously Presented) The method of claim 1, wherein the patient sample nucleic acid comprises multiple segments containing different loci.

20. (Previously Presented) The method of claim 19, wherein the multiple segments containing different loci are affixed to the same microarray site.

21. (Withdrawn- Previously Presented) The method of claim 19, wherein the multiple segments containing different loci are affixed to the different sites.

22. (Previously Presented) The method of claim 6, wherein the multiple patient samples are provided on multiple sites of the microarray.

23. (Previously Presented) The method of claim 1, further comprising the steps of:

providing a labeled amplification control that is capable of binding with the patient nucleic acid sample; and

hybridizing the labeled amplification control to the patient nucleic acid sample.

24. (Canceled)

25. (Previously Presented) The method of claim 1, wherein the genetic disease is cystic fibrosis.

26-44. (Canceled)